

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:54:31 ; Search time 13.86 Seconds
(without alignments)
1110.426 Million cell updates/sec

Title: US-09-587-111-5
Perfect score: 4004
Sequence: 1 MTSPSSPVFRLETLDDGGE.....EDEDGASENVVFLQSN 764

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1645.5	41.1	839	4	US-09-197-636-2
2	1644.5	41.1	839	4	US-09-197-636-8
3	1638.5	40.9	839	4	US-09-197-636-4
4	151	3.8	1839	2	US-09-172-977-4
5	150	3.7	1088	4	US-09-083-059-2
6	148	3.7	843	2	US-09-172-977-3
7	146	3.6	1095	4	US-09-112-096-15
8	138.5	3.5	352	3	US-09-065-474-139
9	138.5	3.5	1745	2	US-09-031-485-33
10	138.5	3.5	1745	2	US-08-847-429A-33
11	138.5	3.5	1745	3	US-09-065-474-33
12	137	3.4	1533	1	US-08-623-679-9
13	137	3.4	1533	3	US-08-933-774-9
14	131	3.3	303	2	US-09-031-485-23
15	131	3.3	303	2	US-08-847-429A-23
16	131	3.3	303	3	US-09-065-474-23
17	129	3.2	348	2	US-09-031-485-28
18	129	3.2	348	2	US-08-847-429A-28
19	129	3.2	348	2	US-09-065-474-28
20	127	3.2	300	2	US-08-897-340-32
21	127	3.2	300	4	US-09-252-329-32
22	126	3.1	551	3	US-08-699-103B-25
23	125.5	3.1	787	4	US-09-188-930-334
24	125.5	3.1	1139	1	US-08-537-210A-4
25	125.5	3.1	1139	4	US-09-113-825-4
26	125.5	3.1	2703	1	US-08-185-432-19
27	123.5	3.1	191	2	US-09-031-485-20

28	123.5	3.1	191	2	US-08-847-429A-20	Sequence 20, Appl
29	123.5	3.1	191	3	US-09-065-474-20	Sequence 20, Appl
30	122	3.0	741	3	US-08-943-956A-2	Sequence 2, Appl
31	120.5	3.0	302	2	US-09-031-485-38	Sequence 38, Appl
32	120.5	3.0	302	2	US-08-847-429A-38	Sequence 38, Appl
33	120.5	3.0	302	3	US-09-065-474-38	Sequence 38, Appl
34	120.5	3.0	741	2	US-08-462-481-2	Sequence 2, Appl
35	120.5	3.0	741	2	US-08-436-771-2	Sequence 2, Appl
36	120.5	3.0	741	2	US-08-436-771-4	Sequence 2, Appl
37	120.5	3.0	741	2	US-08-434-998-2	Sequence 2, Appl
38	120.5	3.0	741	2	US-08-434-998-4	Sequence 2, Appl
39	120.5	3.0	741	2	US-08-487-797-2	Sequence 2, Appl
40	120.5	3.0	741	2	US-08-487-797-4	Sequence 2, Appl
41	120.5	3.0	741	2	US-08-701-005A-2	Sequence 2, Appl
42	120.5	3.0	741	2	US-08-479-895-2	Sequence 2, Appl
43	120.5	3.0	741	5	PCT-US95-02058-2	Sequence 2, Appl
44	120.5	3.0	741	5	PCT-US95-02058-4	Sequence 2, Appl
45	119.5	3.0	357	2	US-08-031-538-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-197-636-2
; Sequence 2, Application US/09197636
; Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23, 031
REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-197-636-2

Query Match	41.1%;	Score 1645.5;	DB 4;	Length 839;
Best Local Similarity	48.5%;	Pred. NO. 9.1e-147;		
Matches 344;	Conservative 121;	Mismatches 200;	Indels 45;	Gaps 11;

Oy	74	FDORLFFNAVSRGPEDOLAGLPELVLSTKSTKLTDTSETEGSTGKTCMLKAVNLKQSVNA	1333
Db	113	YDRSIEFAVANOONCCQDLESLLLEFLQSKKHLTDNEKDEPTEKTKCLLKMNLJHDQNT	1722
Oy	134	CILPLQIDRPSGNDOPLVNAQCTDDVYRGCHSAHIAIEKRSLOCYVLLVENGANVARA	1933
Db	173	TIPLELTAIRQDTSKLELVNASTYDSYKQGTALHAIERRNNALYTLUVENGADYQAA	2322
Oy	194	CGRFPQKQOG--TCYFFGELPLSLACTKQMDVSYLLENPHQASLOATDTSQGTUVAHAL	2522
Db	233	HGDFEKKRKGRRGFEGLPLSLACTNOLOIYKFLLONSMOTADISARBSVGTUVAHAL	2922
Oy	253	VMSDNSAENIALATYSMDGLQAGARCLPVOLOEDIRNLQDITPLAKKEGTEIEFRH	3122
Db	293	VEVADNTADNKRFTYSWNEILLIGALHLPRLKBEELTNKKGMPTPLAAGTGTGVLAY	3522
Oy	313	ILOREEFS--GLSHLSRKTEKCYGPRVAVSYLDASVDSCEBNSVLEITIAN--HCKSPHRH	3699
Db	353	ILOREIOPECRHLSRKTEEMAYGPRVHSSYLDSCIDTCKNSVLEYIAVSSSETPRKH	4122
Oy	370	MVLEPRLCKLLQAAKMDLLIPK--FELNFECLNIYVEIFTPAAVAHOPRLKQAAHKLKE-V	4277
Db	413	MLVLEPRLRLLODKMDKPRVKRIEFLNFLVLYCLNIITPMAAYIPV---DGLPEPKMEKT	4699
Oy	428	GNSMLLTGCHILLIGIYLLVGLQVLFWRHRHFWIWSIFDSYREIIEFLFOALLTVVSQVL	4877
Db	470	GDYPRVGEIISYLVGAVYFFFRGLOYFLORRPSKTLFVDSYSMEFLFLOSLTLMATVVL	5299
Oy	488	CEFLAIEWTLPLVSAVLYGNLILYYRGPHQHSISVMLOKYLIRPLREFLILYVEIF	5477
Db	530	XFSHLKEVYASMYVSLALGWTMLYTRGRQOMGTAIVMIEKMLIRPLCFFMYVYVEIF	5699
Oy	548	GPAVALVSLSOEA-----WRPEAPGPNATESVOPMEGDEGNGAQRGIL	5947
Db	590	GFSTAVVLLIEDGKNDLSLPSESTSHRRGPRACRPDSS-----YNSLY	6322
Oy	595	EASLELFEFTTGMEELAFQEOBLHGRGVALLLAVYLTITLLNMILAMSETVSVAT	6547
Db	633	STCELELFEFTTGMDLFEFTETVDKRAVITLLLAIVLLYTLILLNMILAMGETVINKIAO	6922
Oy	655	DSWSITLQKALASVLENGEYMWG--RRKORAGVLTGTGRPDGSPDECRMFCEVEYVMAAS	7133
Db	693	ESKNIMKLORAITITLIDPEKSFCLKMRAPRSRGLQGYTPDGKDDYRWGCFRVDENVMTT	7522
Oy	714	WEOTLPLTLCBPSGA--GVPRILENPVLASPKEDDGCASEENTVPVQOLQ	7627
Db	753	WNTVANGIINEDPGNCEGVKRLTSLSKSS---RVSGRHKMKNALVPLLR	7987

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: IBM Diskette
3 COMPUTER: IBM Compatible
4 OPERATING SYSTEM: DOS
5 SOFTWARE: FASTSEQ for Windows Version 2.0
6
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/09/197,636
9 FILING DATE: 23-NOV-1998
10
11 CLASSIFICATION:
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13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: UK 9805137.8
15 FILING DATE: 12-MAR-1998
16 APPLICATION NUMBER: UK 9815791.0
17 FILING DATE: 21-JUL-1998
18 APPLICATION NUMBER: UK 9819278.4
19 FILING DATE: 03-SEP-1998
20
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Prestia, Paul F
23
24 REGISTRATION NUMBER: 23,031
25 REFERENCE/DOCKET NUMBER: GP-30075
26
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 601-407-0700
29 TELEFAX: 610-407-0701
30
31 TELEX: 846169
32
33 INFORMATION FOR SEQ ID NO: 8:
34
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 839 amino acids
37 TYPE: amino acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40
41 MOLECULE TYPE: protein
42
43 US-09-197-636-8

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[illegible]


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      APPLICATION NUMBER: US/08/847,429A
      FILING DATE: 24-APR-1997
      CLASSIFICATION: 435
      ATTORNEY/AGENT INFORMATION:
      NAME: Verser, Carol Talkington
      REGISTRATION NUMBER: 37,459
      REFERENCE/DOCKET NUMBER: HM-5
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 970/493-1772
      TELEFAX: 970/484-9505
      INFORMATION FOR SEQ ID NO: 33:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1745 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      US-08-847-429A-33

Query Match          3.5%; Score 138.5; DB 2; Length 1745;
Best Local Similarity 25.1%; Pred. No. 0.00097;
Matches   59; Conservative   33; Mismatches   84; Indels   59; Gaps    9

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	Query Match:	3.5%	Score	138.5	DB	2	Length	1745
	Best Local Similarity	25.1%	Pred.	No. 0.00097				
Matches	59	Conservative	33	Mismatches	84	Indels	59	Gaps
OY	167	LHAIEKRSLOQCYKLIVENGANVHARACGRFFOKGOGTCFYPGBELPLSLAACKTROMDVS	226					
		: : : : : :						
Db	582	LHVAAHYHNNDKKVALLLLENGASAHAAKN-----	628			-GYTPHLIAAKNKQMDIAS		
OY	227	YLLENPHQPASLQATDSQGNTVLHALVMISDNSAEINALTAYMTDGLQAGARLCPPVOL	286					
		: : : : : :						
Db	629	TLL---HYKANNAANSAKCAFTPLH--LAAEGHREMAAL--LIENGAVAYGAQR-	679					
OY	287	EDIRNLDDLPILKAKEGKIETFRHILQDEFS-----	328			-GISLSRK		
		: : : : :						
Db	676	-----NGLTPMHCIAOEDRVSVAEELVKNNALIDPKTKAGYPLHVACHFGIOINMRFL	729					
OY	329	TEWCYGPVRTSLDIADSVDCSE-----NSVLEITIAFHCKSPRRHRMVLEP LN	377					
		: : : : : :						
Db	730	IE-HG-ARYSVAITRASVPTPLHQAOQGHSVRYLLEHGASFNVHTSTGOPTLS	781					

RESULT 11
US-09-065-474-33 ; Sequence 33, Application US/09065474
; Patent No. 6065999
; GENERAL INFORMATION:
APPLICANT: Tang, Liang

TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKRYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:

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:      TELEPHONE: 970/493-7272
:      TELEFAX: 970/484-9505
:      INFORMATION FOR SEQ ID NO: 33:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 1745 amino acids
:      TYPE: amino acid
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:      US-09-065-474-33

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Query Match	3.5%	Score 138.5	DB 3	Length 1745
Best Local Similarity	25.1%	Pred. No. 0.00097		
Matches 59; Conservative	33;	Mismatches 84;	Indels 59;	Gaps 9

OY	167	LHIAIEKRSLQCVLLENGANNVBARCGRFPKQGCGTCYFEGELPLSTLAACRKHMDYVS	226
Db	582	LHVAAHHNNDKVALLLENGASAHAAAKN-----GTFPHIATKANOMDIAS	628
OY	227	YLLENPHQPASTLOATDSOGNTVLHALWISDNSAENIALVTSMYDGLQAGARLCPPVOL	286
Db	629	TLL--HYKANANESKAGFTPLH-LAAGEGHREMAAL-----LIENGAVYGQAR-675	
OY	287	EDIRNLDDLPFLKAKEGTIEIFRHILQREFS-----GLSHSRKF	328
Db	676	-----NGLPTPMHLCAQEDRYSAVEELVKEMAAIDPKTKAGYTPLVACHFCGOINNVRL	729
OY	329	TEMCYCPRVRSLYLDASVDSEE-----NSYLEIIAFHCCKSPRRHRMNYLDEPLN	377
Db	730	IE-HG-AARYSVITRASYPPLHQQAQGNHSVRYLLEHSPASPVNHTSGTGPIS	781

RESULT 12

US-08-623-679-9
; Sequence 9, Application US/08623679
; Patent No. 5674739

GENERAL INFORMATION: Andrew M.
APPLICANT: Shyjan,
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR
TITLE OF INVENTION: PROGRESSION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

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;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-623-679-9

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Query Match	3.48;	Score 137;	DB 1;	Length 1533;
Best Local Similarity	19.98;	Pred. No. 0.0011;		
Matches 101;	Conservative 88;	Mismatches 180;	Indels 138;	Gaps 22

[illegible]

RESULT 13

US-08-933-774-9
; Sequence 9, Application US/08933774A
; Patent No. 6025137

```

1  GENERAL INFORMATION:
2  APPLICANT: Shyjan, Andrew W.
3  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
4  TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
5  FILE REFERENCE: 0734/004003
6  CURRENT APPLICATION NUMBER: US/08/933, 774A
7  CURRENT FILING DATE: 1997-09-19
8  EARLIER APPLICATION NUMBER: US 08/623, 679
9  EARLIER FILING DATE: 1996-03-29
10 EARLIER APPLICATION NUMBER: US 08/412, 431
11 EARLIER FILING DATE: 1995-03-29
12 NUMBER OF SEQ. ID NOS: 10
13 SOFTWARE: FastSeq for Windows Version 3.0
14 SEQ. ID NO. 9
15 LENGTH: 1533
16 TYPE: prt
17 ORGANISM: Homo sapiens
18 US-08-933-774-9

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SEQUENCE CHARACTERISTICS:	Query Match	3.48	Score 137	DB 3	Length 1533
LENGTH: 1533 amino acids	Best Local Similarity	19.96	Pred. No. 0.0011		
TYPE: amino acid	Matches 101: Conservative	88	Mismatches 180	Indels 138	Gaps 22


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-847-429A-23

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Query Match	Score	DB 2;	Length
3.38;	131;		303;
39.04;	0	0.00021	

QY	139	LOIRDSONPOPLVNAACSTDYUHGSAHIAIEKRSJLCCVKLLV-----ENGAN	188
		: :	
Db	26	LLDR-----NADP--NARLN-----GTPPLHACKKNKIKVELLKKHAAIEATESGSL	76
QY	189	-VHARACGRFOKGOGTCFYF-----GELPLSLAACKOMDVSYLLENPHQ	234
Db	77	PLHVA-----FMGAINIYIYLQOGANADVATVGETPLHLAARAOQTDIVRYLVNR--	129
QY	235	PASVQATDSOGNTFLHMLVMSDSASAINALVMSYMGILLQAGRLCEPYQLEDIRLQD	234
Db	130	GAQVDAARRELQTPHLASRIGN-----TDIVLLQDANK--SPNATRDV-----	173
QY	295	LTPPLKAKEKIEIFRHIL-----QREPSGLSHLSRKTEWCYC--EVRVSLYD	342
Db	174	YTPPLHAAKEGEEVVAALIMDHGTDTLLTKKGTPL-HIAAK-----YGNLPVANSLE	227
QY	343	LAS--VDSCENSYLEI-TAFH 361	
Db	228	RGTVPDIEGKNQVTPPLHVAH 248	

Search completed: July 18, 2001, 15:59:03
Job time: 272 sec

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